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| ALS29018 ALS29050 | ITL NFL008 TO AUT 1978 AUT 3978 NITRP3 HOME S ALS299050 | ITL NFL008 TO AUT 1978 AUT 3978 NITRP3 HOME S ALS299050 | ITL NFL000 LNH ALS299050 | ITL NFL000 LNH ALS299050 | ITL NFL000 LNH AUT 300 AUT 37008 LITL NFL000 LNH AUT 300 AUT 3700 B LITL NFL001 LNH AUT 300 AUT 3700 B LITL NFL001 LNH AUT 300 AUT 3700 AUT 3700
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ALE998R5 ALE29895 III_MPLOOLNH
BI145391 602910754F1 H71_G8AF_U
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| REMICHEL POS BTOCSO 281100-118-
| PG745818 6027239633 | NIH_MOC_1
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- 0-1/cmn2 | Jusepte - proof / Unserpte | DEV-x1p
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- 0-1/cmn2 | Jusepte - proof / Unserpte | DEV-x1p
- UN-MST - QEMT-fastap - SUFFIX 1SL - GAPOP-12, 000 - GAPOP-4, 000
- MINMATCH-0.100 - LOOPEL-0.000 - LOOPEXT-0.000 - QGAPOP-4, 500
- GGAPEXT-0.000 - LOOPEL-0.000 - NGAPEXT-0.500 - PGAPOP-4, 000
- GGAPEXT-0.000 - STARF-0.000 - NGAPEXT-0.500 - PGAPOP-6, 000
- PGAPEXT-7, 000 - STARF-0.000 - NGAPEXT-0.500 - DELDE-b.000
- DELEXT-7, 000 - STARF-0.000 - THR_MATX-100 - THR_MIN-0
- ALLIGN-15 - MODEL-LOCAL - OUTHAM-PPE - NORM-CXL - MINLEN-0
- MAXEN-2000000000 - USER-US09525998 - GCGM_1 - 3998 - NCPU-6
- ICPU-3 - LONGLOG - NO_XLPXY - WALT - THREADS-1
                                                                                                                        About: Results were produced by the GenCore software, version 4.5,
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Ouery length: 455
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qb_est2:BG680356
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ab_est2:BF839822
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BIRTHAGKA GASPAGOSTA NIL_CGA
BERTORY 115-010149-991100 E
BILSSELS (CTTP526351 ATH_M32
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Note: The control of the control of the control of the state of the control 
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Bukaryora, Morazoa; Chordara; Catarrhini; Hominidae; Homo.
1 (bases 1 to 957)
Li.W.B., Gruber,C., Tessee,J. and Polayes,D.
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Email: Segret Geooscope costil. Neb : www.genoscope.rns.fr.
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/clone="CSobJAllOYE05"
/clone=lb="III-NFL008_IG2"
/sex="male"
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773.60 1044.72
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AL559050.1 01:12904166
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Ratio: 5.575
Percent Similarity, 99.608
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gb_est2.BG698459
gb_est2:B1414468
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gb_est1:8F807089
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84 ysGluSerClySerPheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
                                                                                                                     101 SerCysSerLysCysArqLysCluMetGlyGlnValGluIleSerSerCy 117
                                                                                                                                                                                                                                                                                      117 sThrValAspArgAspThrValCysClyCysArglysAsmClnTyrArgH 134
                                                                                                                                                                                                                                                                                                                                 543 CACAGIGGACCGGGACACCGIGGGGGGGACAGAAGAAGAAGAAGAAGGGG 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 rleuTyrAsnAspCysProClyProClyClnAspThrAspCysArgCluC 84
                                                                                                                                                                                                                                                                                                               251 SerThrProGluLys 255
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Homo sapiens Bukaryota: Mctazca, Chordata, Craniata, Vertebrata: Enteleustumi, Mammalia: Entheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 761) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Naqai,T., Sugano,S. and seq_documentation_block: LOCUS AUT31978 751 hp nPNA EST 24.0CT 2000 DEFINITION AUT31978 NT2RP3 Homo sapiens cDNA clone NT2RP3003570 5', mRNA 1532-4 Yana, Kisarazo, Chiba 292 0812, Japan Tel: 81-438-52-3951 Helix Research Institute AU131978 AU131978.1 GI:10992332 HRI human coNA project Contact: Takao Isogai Genomics Laboratory Unpublished (2000) seducuco Isodai, T human. EST. ORGANISM ACCESS 10N REFERENCE AUTHORS JOURNAL. KEYWORDS VEPSION TITLE COMMENT SOURCE

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Fax: 81-438-52-3952
Email. genomics@hti.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Pengarch Institute; cDNA library construction. Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AGCTGCTCCAAATGCCGAAAAGGAAATGGGTCAGGTGGAGATCTCTTG 411
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                                                                                                                                            /organism-"Homo sapiens"
/db_xref-"Laxon:9606"
/clone-"NT2RP3003570"
                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               5.489
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284 GCTGTTGGTGGGAATALACCCCLCAGGGGTLALIGGACTGGCCCTCACC 333

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Anothal Torque: brain; Vector: pcMVSPORT 6; 1st strand cDNA was primed with a North-olign(dT) primer. Five prime condensitioned double-stranded cNNA was digested with Not 1 and cloned into the Not 1 and Eco RV sites of the pcMvSnopr 6 by Life Tachnologies. Contact. From Limia Life by Life Tachnologies. Contact. From Limia Life British Contact. From Limia Life British Contact. From Limia Life British Drive Econologies, a division of Invitrogen 9800 Medical Center Drive Econologies, a division of Invitrogen 9800 Medical Center British Entitle Mary and 20859, USA Fix. (1) 301-519 BRITISH Entitrogen Contact British Limia Filiangel Freech.com URL.:
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                       LOCUS ALS29836 912 bp mRNA EST 13.FEB.2001
DEFINITION ALS29836 LTI_NFL001_NBC4 Homo sapiens cDNA clone CSODD005YP05 5
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                           234 ATGGGCCTCTCTCACCTGACCTGACTGCTGCTGCTGGTGCTGCTGCTGTGCTGGA 283
                                                                                                 201 AsnValLysGlyThrGluAspSerGlyThrThrVal.LeuLeuProLeuV 217
                                                                                                                                                                                                                                                     712 NCATITICITIGGICTITGCCHITTAICCCINCTCTICATIGGHTAATG 761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Lissue_type-"neuroblastoma_cells"
/lab_host-"DHIOR"
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/db_xrel-"taxon:9606"
/elone-"csubb005vpns"
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AL529836
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Li,W.B., Gruber,C.,
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Ratio: 5.389
milarity: 98.734
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17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL 34

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Bukaryota; Metazoa; Chordata; Graniata; Vertebrata: Enteleostomi;
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1 (bases 1 to 975)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 CACCCICAAAAIAAITGGATTIGCIGIAGGAAGIGCCACAAAGGAACGIA 433
                                                                                                                                                    434 CITGIACAATGA TGICCAGGCCCGGGGGAAAGAIAGGGACT 483
34 euglyAspArd) ulySArgAspSerValCySProGlmCyTystyrile 50
                                                                                                                        67 rleufyrAsnAspCysProGlyProGlyClnAspFhrAspCysArgGluC 84
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167 rCysHisAlaGlyPhePheLeuArqGluAsnGluCysValSerCysSerA 184
                                                                                                                                                                                       Another "Verfer pawyshorr 6, Site_1, Noti, 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco PV sites of the pawyspopt 6
                                                                                                                                                                                                                                                                          Email: seqret@qenoscope.cns.tr, Web : www.qenoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           406 CACCCTCAAAATAATTCGATTTGCTGTACCAAGTGCCACAAAGGAACCTA 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 isTyrTrpSerGluAsnLeuPheGlnCysPheAsnCysSerLeuCysLeu 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 ysGluSerGlySerFheThrAlaSerGluAsnHisLeuArgHisCysLeu 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 SorrysSorrysParglysGlyMorralys/10141019110SorSorScripy 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                606 CACACTGGACGGGACACCGTGTGTGCTGCAGGAAGAACCAGTACCGGC 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          656 ATTAITGGAGTGAAAACCITITCCAGTGCTTCAAITGCAGCCTCTGCTC 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 AsnClyThtValHisLeuSerCysClnGluLysGlnAsnThrValCysTh 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 uLeuLeuValGlyIleTyrProSerGlyValIleGlyLeuValProHisL 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 euGlyAspArqCluLysArqAspSerValCysProGlaGlyLysTyrIle 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 HisProCinAsnAsnSerlleCysCysThrLysCysHisLysClyThrTy 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 rLeuTyrAsnAspCysProGlyFroGlyGlnAspThrAspCysArqGluC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity, 95 R16
                                                                                                                        /clone "CS0DIGBZYA01"
/clone_lib="LTI_NFL006_PL2"
/rissuo_fype "placenta"
/mate "Vertor pOMVSHORY 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alian seq 1/1 to: AL577008 from: 1 to: 975
                                                                                     /orqanism-"Homo sapions"
BP 191 91006 EVRY cedex - France
                                                                                                         /db_xret-"taxon:9606"
                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity: 97.071
                                                                975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 1245,50
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                                                                   SOUTCE
                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                            FEATURES
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/note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: Noti: Site_2: Sall; Cloned unidirectionally; oligo-di primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Lile Terhnologies. Note: Lihis is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 974)
MIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health; Mammalian Gene Collection (MGC) Impublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602329676F1 NIH_MGC_91 Home supiens cDNA clone IMA3E.44 NB19 57, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by. The I.M.A.W.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Consortium (LLNL) Clone distribution: MGC clone distribution information can be found through the I M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-FEB:2001
                                                                                                                                       | HITHTHITHITHITHITHITHIT | SECOND CONTRACTOR | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 150 | 
217 alilePhePheGlyLeuCysLeu.LeuSerLeuLeuPheIleGlyLeuMe 233
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/Lissue_type="adenocarcinoma, cell line"
/lab_host-"DH10B (phaqe-resistant)"
                                                                                                                                                                                                                                                                                                                                     200 uAsnVallysClyThrCluAspSerGlyThrThrVall.culeuProleeV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 657.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone-"IMAGE:4431019"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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98.276
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US-09-525-998A-2 x BG180101
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KEYWORDS
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Align seg 1/1 to: BC180101 from: 1 to: 974

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251 AGAGGGGTCCTTCACCCTTCACAAAACCACCTCAGAGAGACTGCTTCAGC 300
                                                                                                                                                                                                                                                                                                                                     102 CysSerLycCycArgLysCluMetGlyClnValGluIleSerCysTh 118
                                                                                                                                                                                                                                                                                                                                                  152 GlyThrValHisLeuSerTysGluGluLysGluAsnIhrValTysThrUy 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 luSerGlyserPheThrAlaSerGluAsnHisLeuArqHisCysLeuSer 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                135 yrTrpSerGluAsuLeuPheilm*ysPheAsm;ysSerLeu;ysLeuAsn 151
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                                                      18 of.cuValGlyfleTyrProSerGlyVallleGlyLeuValProHisLeuG 35
                                                                                                          35 lyAspArqGluLysArqAspSerValCysProGlnGlyLysTyrlleHis 51
                                                                                                                                                                                                                       68 uTyrAsnAspCysProClyProClyProClyCluCysG
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Eukaryola; Metawoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 889) seq_decumentation_block: LOCUS AU17362 889 bp mRNA EST 19-OCT-2000 DEFINITION AU17362 HEMBAL Homo sapieus cDNA clone HEMBAL001229 5', mRNA Ota, L., Nishikawa, L., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y. AU117362.1 GI:10932324 seq_name: qb_estl:AU117362 Homo sapiens sequence. AIII 17362 ћитап. EST ORGANISM ACCESSION AUTHORS REFERENCE KEYWORDS VERSION SOURCE

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Email: 4-works this of physics of the second one pass sequencing; Hellx Research Institute; conal library construction; Department of Virology, Institute of Medical Scheme, University of lokyo, and
Yamamoto,J., Wakamatsu,A., Nakamnia,Y., Nagai,T., Sugamo,S. and
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/drope="mainly for 1" access"
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1532-3 Yana, Kisarazu, Chiba 292 0812, Japan
Tel: 81 448-52-4951
Email: 4-modis 941.co.jp
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/organism="Homo saptens"
/h_xn; "Laxon:9606"
/clone="HEMBA1001229"
/clone=11b="HEMBA1"
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                                                                                           HRI human cDNA project
                                                                                                                                   Unpublished (2900)
Contact: Takao Isogai
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Mammallar Eutherla: Primates: Catarrhini; Hominidae; Homo.
1 (bases 1 to 718)
NIH-MGC http://mgc.nci.nih.gov/.
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CDNA Library Arrayod by The I M A P Censertium (ILNI)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution. MGC clone distribution information can befound through the L.M.A.G.E. Consortium/LLNL at:
Plate: LLAM10608 row: b column: 17
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                373 GluPheValArdArdLeuGlyLeuSerAspHisGluIleAspArgLeuGl 389
                                     489 uleuGinAsnGlyArgCysLeuArgGluAlaGinTyrSerMetLeuAlaT 406
                                                                                                                                     503 GETGEAGAAGGGGEGEGEGEGGGGGGGATACAGGTGGGGGA 552
                                                                                                                                                                          406 hrTrpArqArqArqThrProArqArqGluAlaThrLeuGluLeuGly 422
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Tissue Procurement: James Cleaver, M.D.
                                                                                                                                                                                                                                                                                                                                       439 uAlaLouCysGlyProAlaAlaLeuProProAlaPro 451
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/clone-"lMAGE:4751536"
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was primed with a NoLL-ollqo(dT) printer. Five printe end enriched, double-stranded cDNA was digested with Not I and cloned into the NoL I and Eco RV sites of the ptMVSFORI 6 vector— library was constructed
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Rukaryota: Metaroa: Chordata; Cramiata; Vertebrata; Buteleostomi,
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BP 191 91006 EVRY cedex - France
Email: seqrel genoscope ens tr. Web - www genoscope.cns.lr.
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HITHITHIHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
348 CACCCIOAAATAAITAGTGITACGAGGGCACAAAAGAAACTA 397
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                                                                  Li.W.B., Gruber.C., Jessee, J. and Polayes, D. Pull-length cDNA libraries and normalization Unpublished (2001)
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Clone listribution, MGD (lone distribution information can be found through the L.M.A.G.E. Consortiom/ELNL at:
http://mage.lib.go.co.commic.22
Plate: LLAM9574 Frow: o column: 22
High quality sequence stop: 642.
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848 CCAAAAGGC 856

202 TCTCTTCTTGCACASTGGAAAAGAAAAAAAGAGTGTGGGAGAGAAGAAA 251 97 qHisCycLeuSerCysSerLysCysArqLysGluMetGlyGluValGluI 114 114 leSerSerCysThrValAspArgAspThrValCysClyCysArgLysAsn 130 147 rLeuCysteuAsnGlyThrValHisLeuSerGysGlnGluLysGlnAsnT 164 164 hrValCysThrCysHisAlaGlyPhePheLeuArgGluAsnGluCysVal 180 181 SerCysSerAsnCystysSerLeaCluCysThrtysLeaCysteuPr 197 402 TCCTGTAGTAACTGTAAGAAAAGGGTGGAGGAAGTTGTGCCTAGC 451 197 oGlnIleGluAsnValLysGlyThrGluAspSerGlyThrThrValLeuL 214 214 cu.ProtecaValliePhePheClysteuCysteuLeuScrieuLeuPhell 230 502 Teccectestatiteticastricescritiarecetecter 551 230 cGlyt.cuMctTyrArqTyrClnArgTrpttysScrtys.t.cuTyrScrffc 246 263 TThrigsProteuAlaProAstiPro......SetPheSetProT 276 276 hrProdlyPheThrFreShr............289 ThrTyrThrProGlyA 303 303 spCysProAsnPheAlaAlaPro.... ArgArgGluValAlaProPro 317 33 SACTAGACACTGGGAGGACCACCAACGAAAAGGAAGAAAGCAAGAAA 847 81 CysArgCluCysCluSerGlySerPheThrAlaSerCluAsnHisLeuAr 97 48 LysTyrIleHis.ProGlnAsnAsnSerIleCysCysThrLysCysHisL 64 Align seg 1/1 to: HE871809 from: 1 to: 969 290 SerSerThrPheThrSerSer Ser 318 Tyrcincly 320

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Homo sapiens
Eukaryota, Metazda, Cherdata, Chamiata, Veitchnata, Euteleostomi;
Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
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//lab_host="NH10B (phage-resistant)"
//none="Aordan liver; Vertor: pCNV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally; oliqo-dT primed.
Average insert size 1.7 kb. Library enriched for full longth clones and constructed by Life Technologies.
Note: this is a NH-MGC Library."
                                                                       BG035257 636 bp menA ES: 24 JAN 2001 602324771F1 NIH_MCC_90 Homo sapiens conA clone IMAGE:4413112 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Arrayed by: The L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by. Incyte Genemics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                   National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I M A G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 uCluClyThrThrThrLysProLeuAlaProAsnPreSerPheSerProT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism-"Homo sapiens"
/db_xret-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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Location/Qualifiers
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/clone_lib="NIH_MGC_90"
                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cqapbs-remail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                 BG035257.1 GI:12429209
                                                                                                                                                                                                                                                                                                                  (bases 1 to 636)
                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
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US:09-525-998A-2 x BC035257
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seq_name: gb_est2:BG035257
                                                                                                                        mRNA sequence.
                                              seq_documentation_block:
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/clone_lib="NiH_MGC_9]"
/tissue_type "ademorarcinoma, cell line"
/lab_host-"DH10B (phage-resistant)"
/note="organ: prostate, Vector, pcMV SPORT6; Site_1: Not1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryola, Metazoa, Chordata, Craniata, Vertebrata, Buleleostomi,
Mammalia, Eutheria, Primates, Caterrhini, Hominidae, Homo.
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91 Homo sapions chNA clone IMADE 4518690 57,
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NIH-MCC bitp://mgo.com/ rib gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                    301 GACAGGGCCACAAGGCACAGAGGTTAGACATTGAGGCGGGGGGGT 350
                                                                                                                                                                                                                             359 uTyrAlaValValGluAsnValProProLeuArqTrpLysGluPheValA 376
                                                                                                                                                                                                                                                                                                                                                                                 393 OlyArgCysleuArgGluAlaGluTyrSerMetLeuAlaThrTrpArgAr 409
                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LENE at.
http://imaue.linl.gov
Plate: LLAM10413 row-1 column: 19
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Email: cgapbs-r:mail.nih.gov
Tissue Procurement: DCTD/DTP
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/clone="!MAGE:4518690"
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RG282718
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Site_2: Sall: Cloned unidirectionally, bilao-dI primed. Average insert size 1.4 kb. Library entidled for full tength clones and constructed by hife technologies. In this is a NHEMBO library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 TGCA3GAAJAA,CAATATTATTAJAJAJAAAASCTTTTAJAJA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 AsndinCysVaiSerCysSer. AsndystystysSert.euGlorysthii 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        259 aGluClyThrThrThrLys.ProlemAlaFrcAsaFroSerFlaSerFro. 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              527 TGAAGGAACTACTACTAATGCCCTGGCCCAAAACTCAAGGTTCAGTCTT 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 GGAIAGGGAGIG AGIGGAGIGIGAGAGGGTIGGIGGIGGGGGGGGAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102 AACCAGCTICAGACACTGOCTCAGACTGCTACAATGTCGAAAGGAAATGG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                            77 nAspibraspijsatg.Gludysdluserdlyserbledlualaserdlu 93
                                                                                                                                                                                                                                                                                                                                                                                                      2 AAGIGGGACAAAGGAAGGIACTIGIAGAAIGAGIGIGGAGGGGGGGGA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS2 CTICAATTOCAGCCCTCTOATTOCAGCCCGCACTCCCACTCCCACC
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                                                                                                                                                                                 Lenath: 285
Cals:
Percent Identity: 78.596
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align and 1,7 to 84282718 from 1 to, 761
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Percent Similarity: 83.860
                                                                                                                                                                                                                                                               alignment_block;
US-09-525-998A-2 x M3282718
                                                                                                                                                                               Ouality: 1110.50
Ratio: 4.545
                                                                                0.00
                                                                                                                                                                alignment_scores:
                                                                                HASE COUNT
                                                                                                     ORIGIN
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275 remarkredlypheThrProThrLeuGlyPheScrProValProSerSer

292 ThrPheThrSerSerSerThrTyrThrProGlyAspCysProAsnPheAl 308

152 ACCTTCACCTCCAGCTCCACCTATACCCCGGTGACTGTGCCAACTTTGC

52 GCTTGAAGGAACTACTACTAACCCCTGGCCCAAACCCAAGCTTCAGTC 101

308 aAlaProArgArgCluValAlaProProTyrClECTyAlaAspProlleL 325

342 GluAspSerAlaHisLysProGlnSerLeuAspThrAspAspProAlaTh 358

375 alArgArgLeuGlyLeuSerAspHisGlulleAspArgLeuGluLeuGln 391 408 gargargThrProArg.ArgGluAlaThrLeuGluLeuLeuGlyArqVal 424

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seg_name: qb_cst2:BG680356

425 LeuArgAspMetAspLeuLeuGlyCysLeuGluAspFleGluGluAlaLe 441

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Anothe-Torqan brain: Vector: pCMVSPORT 6: 1st strand cDNA was primed with a NotL offgo(di) primer. Five prime end curiched, double stranded cDNA was digested with Not L and cloned into the Not L and Bro NV Siros of the pCMVSPORT everor. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liand Library Products and Peng Library Products and Peng
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Mammalia: Eutheria: Primates, Catarrhini, Hominidae, Homo.
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                                                       674 GGCTCCCCCCCCAAGAAAGTT49GTACTAATAAGGGGC TGACCCAT 720
292 rPhethrserSerSerThrTyrThr.ProGlyAspCysProAsnPhe... 307
                                                                                                                                                                                                                 308 AlaAlaProArgArgGluValAlaProProTyrGlnGlyAlaAspProIl 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 769)
Li,W. B., Gruber,C., Jessec,J. and Polayes,D.
Pell - length cluM libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                            324 eleuAlaThrAlaLeuAlaSerAspProfleProAsnProLeu 338
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/sex="male"
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/db_xret-"taxon:9606"
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EST 01-MAY 2001
EGG-CARACAT NCL_CGAL_Skir4 Homo sapiens china clone IMACH.4753981-57,
manna sequence.
                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation. Life Technologies, Inc. LDNA Library Ariayed by. The L.M.A.S.E. Consortion (LLNL) DNA Sequencing by: Inc. Clone distribution: MGC clone distribution; information can be found through the L.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                  NIH-MGC http://mqc.nci.nih.qov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                         Tissue Procurement: James Cleaver, M.D.
                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                   BG680356.1 GI:13911753
                                                                                                                                                                                                                                                                   (bases 1 to 643)
                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
seq_documentation_block:
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                                                                                             BG680356
                                                                                                                                                                      human.
                                          NOT LINEARI
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                                                                                                                                                                   SOURCE
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                                                                                                                                                                                                                                       Length:
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5.204 99.070

Quality: 1108.50

Ratio:

Percent Similarity:

alignment_block: US-U9-525-998A:2 x AL522226

Plate: LLAM10614 row: h column: 14

http://image.llnl.gov

258 uLeuGluGlyThrThrLysProLeuAlaProAsnProSerPheSerP 275

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Ratio: 5.163 Gaps: 2
Percent Similarity: 99-113 Popront 14605117, 97-642
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                                                                                                                                                           /ordanism-"Homo sapiens"
High quality sequence stop: 630.
Location/Qualifiers
                                                                                                                                                                                                  /db_xrel-"Laxon. 3666"
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Eukaryota: Motazoa; Cherdata; Craniata: Vertebiata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
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14.7. Wakamalis, A. Charak, M., Iskii, S., Sait, E., Manamoto, J.,
Nakamura, Y., Nishikawa, T., Nadal, T., Saiakki, Y., Sugano, S., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genomicsthri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix
                                                                                                                                                                                                                  LOCUS AU125-021 845 bp mBNA EST EST 2000
PETINITYN AU125-01 NIDRAG BONG SAGIEGO CDNA (1016 NIDRAGO-00896-55) mRNA
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1832-3 Yana, Kisararu, Chiba 292-esi2, Japan
761, 81 418 52-3951
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29Exret "tax:0:9606"
Zelone:"N12EM4000896"
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HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii.S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Naqai,T., Suzuki,Y., Sugano,S., Isoqai,T.)
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Eukaryota: Metarca: Cherdata: Craniata, Vertebrata, Euteleestomi,
Mammalia: Butheria: Primates; Catarrhin; Hominidae; Homo.
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HRI buman cDNA project, 5 - 6 3'-end one pass sequencing: Helix
Research Institute of SNA library curstraction impartment of
Virology, Institute of Medical Science, University of Tokyo, and
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Nakamura,Y., Nishikawa,T., Nagai,T., Su-uki,Y., Sugano,S. and
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51 HisProGlnAsnAsnSerIleCysCysThrLysCycHisLysGlyThrTy 67
                                                                                      67 rLeuTyrAsaAspCysProGlyProGlyGlaAspThrAspCysArqGluC 84
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Tel: 81-438-52 3951
Fax: 81-438-52-3952
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Genomics Laboratory
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SOURCE

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/cell_type="textcoarcinoma"
/cell_ine="NTS"
/note="Vector: pME188FL3; mkNA from uninduced N12 neuronal
precisor cells"
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                                                                                      /organism="Homo sapiens"
/db_xref+"taxon:9606"
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